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SEQUENCE LISTING

<110> Fletcher, Jonathan A.
Kroll, Todd G.

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AND POLYPEPTIDES AND USES THEREOF

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<150> US 60/177,109

<151> 2000-01-20

<150> US 60/225,079

<151> 2000-08-14

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775

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ttt ggg cgg atg cca cag gcc gag aag gag aag ctg ttg gcg gag atc	1680
Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu Ile	
545 550 555 560	
tcc agt gat atc gac cag ctg aat cca gag tcc gct gac ctc cgg gcc	1728
Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg Ala	
565 570 575	
ctg gca aaa cat ttg tat gac tca tac ata aag tcc ttc ccg ctg acc	1776
Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu Thr	
580 585 590	
aaa gca aag gcg agg gcg atc ttg aca gga aag aca aca gac aaa tca	1824
Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys Ser	
595 600 605	
cca ttc gtt atc tat gac atg aat tcc tta atg atg gga gaa gat aaa	1872
Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp Lys	
610 615 620	

atc aag ttc aaa cac atc acc ccc ctg cag gag cag agc aaa gag gtg	1920
Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu Val	
625 630 635 640	
gcc atc cgc atc ttt cag ggc tgc cag ttt cgc tcc gtg gag gct gtg	1968
Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala Val	
645 650 655	
cag gag atc aca gag tat gcc aaa agc att cct ggt ttt gta aat ctt	2016
Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu	
660 665 670	
gac ttg aac gac caa gta act ctc ctc aaa tat gga gtc cac gag atc	2064
Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile	
675 680 685	
att tac aca atg ctg gcc tcc ttg atg aat aaa gat ggg gtt ctc ata	2112
Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile	
690 695 700	
tcc gag ggc caa ggc ttc atg aca agg gag ttt cta aag agc ctg cga	2160
Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg	
705 710 715 720	
aag cct ttt ggt gac ttt atg gag ccc aag ttt gag ttt gct gtg aag	2208
Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys	
725 730 735	
ttc aat gca ctg gaa tta gat gac agc gac ttg gca ata ttt att gct	2256
Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala	
740 745 750	
gtc att att ctc agt gga gac cgc cca ggt ttg ctg aat gtg aag ccc	2304
Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys Pro	
755 760 765	
att gaa gac att caa gac aac ctg cta caa gcc ctg gag ctc cag ctg	2352
Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln Leu	
770 775 780	
aag ctg aac cac cct gag tcc tca cag ctg ttt gcc aag ctg ctc cag	2400
Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu Gln	
785 790 795 800	
aaa atg aca gac ctc aga cag att gtc acg gaa cac gtg cag cta ctg	2448
Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu Leu	
805 810 815	
cag gtg atc aag aag acg gag aca gac atg agt ctt cac ccg ctc ctg	2496
Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu Leu	
820 825 830	
cag gag atc tac aag gac ttg tac tag	2523
Gln Glu Ile Tyr Lys Asp Leu Tyr *	
835 840	

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Gly	Gly	Ala	Phe	Val	Asn	Gly	Arg	Pro	Leu	Pro	Glu	Val	Val	Arg	Gln	20	25	30	
Arg	Ile	Val	Asp	Leu	Ala	His	Gln	Gly	Val	Arg	Pro	Cys	Asp	Ile	Ser	35	40	45	
Arg	Gln	Leu	Arg	Val	Ser	His	Gly	Cys	Val	Ser	Lys	Ile	Leu	Gly	Arg	50	55	60	
Tyr	Tyr	Glu	Thr	Gly	Ser	Ile	Arg	Pro	Gly	Val	Ile	Gly	Gly	Ser	Lys	65	70	75	80
Pro	Lys	Val	Ala	Thr	Pro	Lys	Val	Val	Glu	Lys	Ile	Gly	Asp	Tyr	Lys	85	90	95	
Arg	Gln	Asn	Pro	Thr	Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	Arg	Leu	Leu	100	105	110	
Ala	Glu	Gly	Val	Cys	Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	Ser	Ser	Ile	115	120	125	
Asn	Arg	Ile	Ile	Arg	Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met	130	135	140	
Asp	Ser	Cys	Val	Ala	Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile	145	150	155	160
Pro	Ser	Ser	Ala	Val	Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu	165	170	175	
Gly	Ser	Thr	Tyr	Ser	Ile	Asn	Gly	Leu	Leu	Gly	Ile	Ala	Gln	Pro	Gly	180	185	190	
Ser	Asp	Lys	Arg	Lys	Met	Asp	Asp	Ser	Asp	Gln	Asp	Ser	Cys	Arg	Leu	195	200	205	
Ser	Ile	Asp	Ser	Gln	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg		210	215	220	
Thr	Asp	Ala	Phe	Ser	Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe	225	230	235	240
Glu	Arg	Gln	His	Tyr	Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys	245	250	255	
Gly	Glu	Gln	Gly	Leu	Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp	260	265	270	
Asp	Gly	Lys	Ala	Thr	Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn	275	280	285	
Leu	Ser	Thr	His	Gln	Thr	Tyr	Pro	Val	Val	Ala	Asp	Pro	His	Ser	Pro	290	295	300	
Leu	Ala	Ile	Lys	Gln	Glu	Thr	Pro	Glu	Val	Ser	Ser	Ser	Ser	Ser	Thr	305	310	315	320
Pro	Cys	Ser	Leu	Ser	Ser	Ser	Ala	Leu	Leu	Asp	Leu	Gln	Gln	Val	Gly	325	330	335	
Ser	Gly	Val	Pro	Phe	Asn	Ala	Phe	Pro	His	Ala	Ala	Ser	Val	Tyr		340	345	350	
Gly	Gln	Phe	Thr	Gly	Gln	Ala	Leu	Ser	Glu	Met	Thr	Met	Val	Asp		355	360	365	
Thr	Glu	Met	Pro	Phe	Trp	Pro	Thr	Asn	Phe	Gly	Ile	Ser	Ser	Val	Asp	370	375	380	
Leu	Ser	Val	Met	Glu	Asp	His	Ser	His	Ser	Phe	Asp	Ile	Lys	Pro	Phe				

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Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp Ile						
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Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu						
	420		425		430	
Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro						
	435		440		445	
Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu						
	450		455		460	
Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys						
	465		470		475	
Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly						
	485		490		495	
Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys Asp						
	500		505		510	
Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr Cys						
	515		520		525	
Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile Arg						
	530		535		540	
Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu Ile						
	545		550		555	
Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg Ala						
	565		570		575	
Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu Thr						
	580		585		590	
Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys Ser						
	595		600		605	
Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp Lys						
	610		615		620	
Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu Val						
	625		630		635	
Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala Val						
	645		650		655	
Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu						
	660		665		670	
Asp Leu Asn Asp Gln Val Thr Leu Lys Tyr Gly Val His Glu Ile						
	675		680		685	
Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile						
	690		695		700	
Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg						
	705		710		715	
Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys						
	725		730		735	
Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala						
	740		745		750	
Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys Pro						
	755		760		765	
Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln Leu						
	770		775		780	
Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu Gln						
	785		790		795	
Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu Leu						
	805		810		815	
Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu Leu						
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Gln Glu Ile Tyr Lys Asp Leu Tyr						

835

840

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gga ggg gcc ttt gtg aat ggc aga cct ctg ccg gaa gtg gtc cgc cag	96
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln	
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cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc gac atc tct	144
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser	
35 40 45	
cgc cag ctg cgc gtc agc cat ggc tgc gtc agc aag atc ctt ggc agg	192
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg	
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tac tac gag act ggc agc atc cgg cct gga gtg ata ggg gcc tcc aag	240
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys	
65 70 75 80	
ccc aag gtg gcc acc ccc aag gtg gtg gag aag att ggg gac tac aaa	288
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys	
85 90 95	
cgc cag aac cct acc atg ttt gcc tgg gag atc cga gac cgg ctg ctg	336
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu	
100 105 110	
gct gag ggc gtc tgt gac aat gac act gtg ccc agt gtc agc tcc att	384
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile	
115 120 125	
aat aga atc atc cgg acc aaa gtg cag caa cca ttc aac ctg cct atg	432
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met	
130 135 140	
gac agc tgc gtg gcc acc aag tcc ctg agt ccc gga cac acg ctg atc	480
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile	
145 150 155 160	
ccc agc tca gct gta act ccc ccg gag tca ccc cag tcg gat tcc ctg	528
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu	
165 170 175	

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Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly	
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agc gac aag agg aaa atg gat gac agt gat cag gat agc tgc cga cta	624
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu	
195 200 205	
agc att gac tca cag agc agc agc agc gga ccc cga aag cac ctt cgc	672
Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg	
210 215 220	
acg gat gcc ttc agc cag cac cac ctc gag ccg ctc gag tgc cca ttt	720
Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe	
225 230 235 240	
gag cgg cag cac tac cca gag gcc tat gcc tcc ccc agc cac acc aaa	768
Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys	
245 250 255	
ggc gag cag ggc ctc tac ccg ctg ccc ttg ctc aac agc acc ctg gac	816
Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp	
260 265 270	
gac ggg aag gcc acc ctg acc cct tcc aac acg cca ctg ggg cgc aac	864
Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn	
275 280 285	
ctc tcg act cac cag acc tac ccc gtg gtg gca gat cct cac tca ccc	912
Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro	
290 295 300	
ttg gcc ata aag cag gaa acc ccc gag gtg tcc agt tct agc tcc acc	960
Leu Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser Ser Thr	
305 310 315 320	
cct tgc tct tta tct agc tcc gcc ctt ttg gat ctg cag caa gtc ggc	1008
Pro Cys Ser Leu Ser Ser Ser Ala Leu Leu Asp Leu Gln Gln Val Gly	
325 330 335	
tcc ggg gtc ccg ccc ttc aat gcc ttt ccc cat gct gcc tcc gtg tac	1056
Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala Ser Val Tyr	
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ggg cag ttc acg ggc cag gcc ctc ctc tca ggg cga gag atg gtg ggg	1104
Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Gly Arg Glu Met Val Gly	
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ccc acg ctg ccc gga tac cca ccc cac atc ccc acc agc gga cag ggc	1152
Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly	
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Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Glu Met Thr Met	
385 390 395 400	

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Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys	
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Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu	
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Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr	
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Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala	
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Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His	
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Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly	
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Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys	
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Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg	
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Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln	
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565 570 575	
atc agg ttt ggg cgg atg cca cag gcc gag aag gag aag ctg ttg gcg	1776
Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala	
580 585 590	
gag atc tcc agt gat atc gac cag ctg aat cca gag tcc gct gac ctc	1824
Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu	
595 600 605	
cgg gcc ctg gca aaa cat ttg tat gac tca tac ata aag tcc ttc ccg	1872
Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro	
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aat ctt gac ttg aac gac caa gta act ctc ctc aaa tat gga gtc cac Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His 705 710 715 720	2160
gag atc att tac aca atg ctg gcc tcc ttg atg aat aaa gat ggg gtt Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val 725 730 735	2208
ctc ata tcc gag ggc caa ggc ttc atg aca agg gag ttt cta aag agc Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser 740 745 750	2256
ctg cga aag cct ttt ggt gac ttt atg gag ccc aag ttt gag ttt gct Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala 755 760 765	2304
gtg aag ttc aat gca ctg gaa tta gat gac agc gac ttg gca ata ttt Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe 770 775 780	2352
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aag ccc att gaa gac att caa gac aac ctg cta caa gcc ctg gag ctc Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu 805 810 815	2448
cag ctg aag ctg aac cac cct gag tcc tca cag ctg ttt gcc aag ctg Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu 820 825 830	2496
ctc cag aaa atg aca gac ctc aga cag att gtc acg gaa cac gtg cag Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln 835 840 845	2544

cta ctg cag gtg atc aag aag acg gag aca gac atg agt ctt cac ccg 2592
 Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro
 850 855 860

ctc ctg cag gag atc tac aag gac ttg tac tag 2625
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 35 40 45
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 50 55 60
 Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys
 65 70 75 80
 Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys
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 Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu
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 Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile
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 Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met
 130 135 140
 Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile
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 Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu
 165 170 175
 Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly
 180 185 190
 Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu
 195 200 205
 Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg
 210 215 220
 Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe
 225 230 235 240
 Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys
 245 250 255
 Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp
 260 265 270
 Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn
 275 280 285
 Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro
 290 295 300
 Leu Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser Ser Ser Thr
 305 310 315 320
 Pro Cys Ser Leu Ser Ser Ser Ala Leu Leu Asp Leu Gln Gln Val Gly

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Ser	Gly	Val	Pro	Pro	Phe	Asn	Ala	Phe	Pro	His	Ala	Ala	Ser	Val	Tyr
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Pro	Thr	Leu	Pro	Gly	Tyr	Pro	Pro	His	Ile	Pro	Thr	Ser	Gly	Gln	Gly
	370					375				380					
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Val	Asp	Thr	Glu	Met	Pro	Phe	Trp	Pro	Thr	Asn	Phe	Gly	Ile	Ser	Ser
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Pro	Phe	Thr	Thr	Val	Asp	Phe	Ser	Ser	Ile	Ser	Thr	Pro	His	Tyr	Glu
		435					440					445			
Asp	Ile	Pro	Phe	Thr	Arg	Thr	Asp	Pro	Val	Val	Ala	Asp	Tyr	Lys	Tyr
	450					455					460				
Asp	Leu	Lys	Leu	Gln	Glu	Tyr	Gln	Ser	Ala	Ile	Lys	Val	Glu	Pro	Ala
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Ser	Pro	Pro	Tyr	Tyr	Ser	Glu	Lys	Thr	Gln	Leu	Tyr	Asn	Lys	Pro	His
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Glu	Glu	Pro	Ser	Asn	Ser	Leu	Met	Ala	Ile	Glu	Cys	Arg	Val	Cys	Gly
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Asp	Lys	Ala	Ser	Gly	Phe	His	Tyr	Gly	Val	His	Ala	Cys	Glu	Gly	Cys
	515						520					525			
Lys	Gly	Phe	Phe	Arg	Arg	Thr	Ile	Arg	Leu	Lys	Leu	Ile	Tyr	Asp	Arg
	530					535					540				
Cys	Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	Lys	Cys	Gln
545					550					555					560
Tyr	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn	Ala
			565						570					575	
Ile	Arg	Phe	Gly	Arg	Met	Pro	Gln	Ala	Glu	Lys	Glu	Lys	Leu	Leu	Ala
			580					585					590		
Glu	Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp	Leu
		595					600					605			
Arg	Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser	Phe	Pro
	610					615					620				
Leu	Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	Lys	Thr	Thr	Asp
625					630					635					640
Lys	Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	Met	Met	Gly	Glu
			645						650					655	
Asp	Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln	Ser	Lys
			660					665					670		
Glu	Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	Val	Glu
		675					680					6			

770		775		780
Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val				
785		790		795
Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu				800
	805		810	815
Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu				
	820		825	830
Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln				
	835		840	845
Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro				
	850		855	860
Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr				
865		870		

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 <211> 42
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 <213> Homo Sapiens

<220>
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 <222> (3)... (41)

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1 5 10	

<210> 8
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<400> 8	
Thr Tyr Pro Val Val Ala Glu Met Thr Met Val Asp Thr	
1 5 10	

<210> 9
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 <212> DNA
 <213> Homo Sapiens

<220>
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 <222> (3)... (41)

<400> 9	
cg ggc cag gcc ctc ctc tca gaa atg acc atg gtt gac aca g	42
Gly Gln Ala Leu Leu Ser Glu Met Thr Met Val Asp Thr	
1 5 10	

<210> 10
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 <212> PRT

<213> Homo Sapiens

<400> 10

Gly Gln Ala Leu Leu Ser Glu Met Thr Met Val Asp Thr
1 5 10

<210> 11

<211> 42

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (3)...(41)

<400> 11

cc atc gca ggc atg gtg gca gaa atg acc atg gtt gac aca g 42
Ile Ala Gly Met Val Ala Glu Met Thr Met Val Asp Thr
1 5 10

<210> 12

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 12

Ile Ala Gly Met Val Ala Glu Met Thr Met Val Asp Thr
1 5 10

<210> 13

<211> 1372

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (11)...(1363)

<400> 13

gaattcggcg atg cct cac aac tcc atc aga tct ggc cat gga ggg ctg 49
Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu
1 5 10

aac cag ctg gga ggg gcc ttt gtg aat ggc aga cct ctg ccg gaa gtg 97
Asn Gln Leu Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val
15 20 25

gtc cgc cag cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc 145
Val Arg Gln Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys
30 35 40 45

gac atc tct cgc cag ctg cgc gtc agc cat ggt tgc gtc agc aag atc 193
Asp Ile Ser Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile
50 55 60

ctt ggc agg tac tac gag act ggc agc atc cgg cct gga gtg ata ggg	241
Leu Gly Arg Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly	
65 70 75	
ggc tcc aag ccc aag gtg gcc acc ccc aag gtg gtg gag aag att ggg	289
Gly Ser Lys Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly	
80 85 90	
gac tac aaa cgc cag aac cct acc atg ttt gcc tgg gag atc cga gac	337
Asp Tyr Lys Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp	
95 100 105	
cgg ctc ctg gct gag ggc gtc tgt gac aat gac act gtg ccc agt gtc	385
Arg Leu Leu Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val	
110 115 120 125	
agc tcc att aat aga atc atc cgg acc aaa gtg cag caa cca ttc aac	433
Ser Ser Ile Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn	
130 135 140	
ctc cct atg gac agc tgc gtg gcc acc aag tcc ctg agt ccc gga cac	481
Leu Pro Met Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His	
145 150 155	
acg ctg atc ccc agc tca gct gta act ccc ccg gag tca ccc cag tcg	529
Thr Leu Ile Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser	
160 165 170	
gat tcc ctg ggc tcc acc tac tcc atc aat ggg ctc ctg ggc atc gct	577
Asp Ser Leu Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala	
175 180 185	
cag cct ggc agc gac aag agg aaa atg gat gac agt gat cag gat agc	625
Gln Pro Gly Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser	
190 195 200 205	
tgc cga cta agc att gac tca cag agc agc agc agc gga ccc cga aag	673
Cys Arg Leu Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys	
210 215 220	
cac ctt cgc acg gat gcc ttc agc cag cac cac ctc gag ccg ctc gag	721
His Leu Arg Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu	
225 230 235	
tgc cca ttt gag cgg cag cac tac cca gag gcc tat gcc tcc ccc agc	769
Cys Pro Phe Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser	
240 245 250	
cac acc aaa ggc gag cag ggc ctc tac ccg ctg ccc ttg ctc aac agc	817
His Thr Lys Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser	
255 260 265	
acc ctg gac gac ggg aag gcc acc ctg acc cct tcc aac acg cca ctg	865
Thr Leu Asp Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu	
270 275 280 285	

ggg cgc aac ctc tcg act cac cag acc tac ccc gtg gtg gca gat cct	913
Gly Arg Asn Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro	
290 295 300	
cac tca ccc ttc gcc ata aag cag gaa acc ccc gag gtg tcc agt tct	961
His Ser Pro Phe Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser	
305 310 315	
agc tcc acc cct tcc tct tta tct agc tcc gcc ttt ttg gat ctg cag	1009
Ser Ser Thr Pro Ser Ser Leu Ser Ser Ser Ala Phe Leu Asp Leu Gln	
320 325 330	
caa gtc gcc tcc ggg gtc ccg ccc ttc aat gcc ttt ccc cat gct gcc	1057
Gln Val Gly Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala	
335 340 345	
tcc gtg tac ggg cag ttc acg ggc cag gcc ctc ctc tca ggg cga gag	1105
Ser Val Tyr Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Gly Arg Glu	
350 355 360 365	
atg gtg ggg ccc acg ctg ccc gga tac cca ccc cac atc ccc acc agc	1153
Met Val Gly Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser	
370 375 380	
gga cag gcc agc tat gcc tcc tct gcc atc gca ggc atg gtg gca gga	1201
Gly Gln Gly Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Gly	
385 390 395	
agt gaa tac tct ggc aat gcc tat ggc cac acc ccc tac tcc tcc tac	1249
Ser Glu Tyr Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr	
400 405 410	
agc gag gcc tgg cgc ttc ccc aac tcc agc ttg ctg agt tcc cca tat	1297
Ser Glu Ala Trp Arg Phe Pro Asn Ser Ser Leu Ser Ser Pro Tyr	
415 420 425	
tat tac agt tcc aca tca agg ccg agt gca ccg ccc acc act gcc acg	1345
Tyr Tyr Ser Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr	
430 435 440 445	
gcc ttt gac cat ctg tag ttgaagctt	1372
Ala Phe Asp His Leu *	
450	

<210> 14
 <211> 450
 <212> PRT
 <213> Homo Sapiens

<400> 14
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 1 5 10 15
 Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln
 20 25 30
 Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser

35	40	45
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg		
50	55	60
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys		
65	70	75
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys		
85	90	95
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu		
100	105	110
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile		
115	120	125
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met		
130	135	140
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile		
145	150	155
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu		
165	170	175
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly		
180	185	190
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu		
195	200	205
Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg		
210	215	220
Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe		
225	230	235
Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys		
245	250	255
Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp		
260	265	270
Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn		
275	280	285
Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro		
290	295	300
Phe Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser Ser Thr		
305	310	315
Pro Ser Ser Leu Ser Ser Ala Phe Leu Asp Leu Gln Gln Val Gly		
325	330	335
Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala Ser Val Tyr		
340	345	350
Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Gly Arg Glu Met Val Gly		
355	360	365
Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly		
370	375	380
Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Gly Ser Glu Tyr		
385	390	395
Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala		
405	410	415
Trp Arg Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Ser		
420	425	430
Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp		
435	440	445
His Leu		
450		

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<211> 1608

<212> DNA
<213> Homo Sapiens

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aattacagca aacccttatt ccatgctgtt atg ggt gaa act ctg gga gat tct 114
Met Gly Glu Thr Leu Gly Asp Ser
1 5

cct att gac cca gaa agc gat tcc ttc act gat aca ctg tct gca aac 162
Pro Ile Asp Pro Glu Ser Asp Ser Phe Thr Asp Thr Leu Ser Ala Asn
10 15 20

ata tca caa gaa atg acc atg gtt gac aca gag atg cca ttc tgg ccc 210
Ile Ser Gln Glu Met Thr Met Val Asp Thr Glu Met Pro Phe Trp Pro
25 30 35 40

acc aac ttt ggg atc agc tcc gtg gat ctc tcc gta atg gaa gac cac 258
Thr Asn Phe Gly Ile Ser Ser Val Asp Leu Ser Val Met Glu Asp His
45 50 55

tcc cac tcc ttt gat atc aag ccc ttc act act gtt gac ttc tcc agc 306
Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr Val Asp Phe Ser Ser
60 65 70

att tct act cca cat tac gaa gac att cca ttc aca aga aca gat cca 354
Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro
75 80 85

gtg gtt gca gat tac aag tat gac ctg aaa ctt caa gag tac caa agt 402
Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu Glu Tyr Gln Ser
90 95 100

gca atc aaa gtg gag cct gca tct cca cct tat tat tct gag aag act 450
Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr
105 110 115 120

cag ctc tac aat aag cct cat gaa gag cct tcc aac tcc ctc atg gca 498
Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser Asn Ser Leu Met Ala
125 130 135

att gaa tgt cgt gtc tgt gga gat aaa gct tct gga ttt cac tat gga 546
Ile Glu Cys Arg Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr Gly
140 145 150

gtt cat gct tgt gaa gga tgc aag ggt ttc ttc cgg aga aca atc aga 594
Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg
155 160 165

ttg aag ctt atc tat gac aga tgt gat ctt aac tgt cgg atc cac aaa 642
Leu Lys Leu Ile Tyr Asp Arg Cys Asp Leu Asn Cys Arg Ile His Lys
170 175 180

aaa Lys 185	agt Ser	aga Arg	aat Asn	aaa Lys	tgt Cys 190	cag Gln	tac Tyr	tgt Cys	cgg Arg	ttt Phe 195	cag Gln	aaa Lys	tgc Cys	ctt Leu	gca Ala 200	690
gtg Val	ggg Gly	atg Met	tct Ser	cat His 205	aat Asn	gcc Ala	atc Ile	agg Arg	ttt Phe 210	ggg Gly	cgg Arg	atg Met	cca Pro	cag Gln	gcc Ala 215	738
gag Glu	aag Lys	gag Glu	aag Lys 220	ctg Leu	ttg Leu	gcg Ala	gag Glu	atc Ile 225	tcc Ser	agt Ser	gat Asp	atc Ile	gac Asp	cag Gln	ctg Leu	786
aat Asn	cca Pro	gag Glu 235	tcc Ser	gct Ala	gac Asp	ctc Leu	cgg Arg 240	gcc Ala	ctg Leu	gca Ala	aaa Lys	cat His 245	ttg Leu	tat Tyr	gac Asp	834
tca Ser 250	tac Tyr	ata Ile	aag Lys	tcc Ser	ttc Phe	ccg Pro 255	ctg Leu	acc Thr	aaa Lys	gca Ala	aag Lys 260	gcg Ala	agg Arg	gcg Ala	atc Ile	882
ttg Leu 265	aca Thr	gga Gly	aag Lys	aca Thr	aca Thr 270	gac Asp	aaa Lys	tca Ser	cca Pro	ttc Phe 275	gtt Val	atc Ile	tat Tyr	gac Asp	atg Met 280	930
aat Asn	tcc Ser	tta Leu	atg Met	atg Met 285	gga Gly	gaa Glu	gat Asp	aaa Lys	atc Ile 290	aag Lys	ttc Phe	aaa Lys	cac His	atc Ile	acc Thr 295	978
ccc Pro	ctg Leu	cag Gln	gag Glu 300	cag Gln	agc Ser	aaa Lys	gag Glu	gtg Val 305	gcc Ala	atc Ile	cgc Arg	atc Ile	ttt Phe	cag Gln	ggc Gly	1026
tgc Cys	cag Gln 315	ttt Phe	cgc Arg	tcc Ser	gtg Val	gag Glu	gct Ala 320	gtg Val	cag Gln	gag Glu	atc Ile 325	aca Thr	gag Glu	tat Tyr	gcc Ala	1074
aaa Lys 330	agc Ser	att Ile	cct Pro	ggt Gly	ttt Phe	gta Val 335	aat Asn	ctt Leu	gac Asp	ttg Leu	aac Asn 340	gac Asp	caa Gln	gta Val	act Thr	1122
ctc Leu 345	ctc Leu	aaa Lys	tat Tyr	gga Gly	gtc Val 350	cac His	gag Glu	atc Ile	att Ile	tac Tyr 355	aca Thr	atg Met	ctg Leu	gcc Ala	tcc Ser 360	1170
ttg Leu	atg Met	aat Asn	aaa Lys 365	gat Asp	ggg Gly	gtt Val	ctc Leu	ata Ile	tcc Ser 370	gag Glu	ggc Gly	caa Gln	ggc Gly	ttc Phe	atg Met 375	1218
aca Thr	agg Arg	gag Glu 380	ttt Phe	cta Leu	aag Lys	agc Ser	ctg Leu	cga Arg 385	aag Lys	cct Pro	ttt Phe	ggt Gly	gac Asp	ttt Phe	atg Met 390	1266
gag Glu	ccc Pro	aag Lys 395	ttt Phe	gag Glu	ttt Phe	gct Ala	gtg Val 400	aag Lys	ttc Phe	aat Asn	gca Ala 405	ctg Leu	gaa Glu	tta Leu	gat Asp	1314

gac agc gac ttg gca ata ttt att gct gtc att att ctc agt gga gac	1362
Asp Ser Asp Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp	
410 415 420	
cgc cca ggt ttg ctg aat gtg aag ccc att gaa gac att caa gac aac	1410
Arg Pro Gly Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn	
425 430 435 440	
ctg cta caa gcc ctg gag ctc cag ctg aag ctg aac cac cct gag tcc	1458
Leu Leu Gln Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser	
445 450 455	
tca cag ctg ttt gcc aag ctg ctc cag aaa atg aca gac ctc aga cag	1506
Ser Gln Leu Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln	
460 465 470	
att gtc acg gaa cac gtg cag cta ctg cag gtg atc aag aag acg gag	1554
Ile Val Thr Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu	
475 480 485	
aca gac atg agt ctt cac ccg ctc ctg cag gag atc tac aag gac ttg	1602
Thr Asp Met Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu	
490 495 500	
tac tag	1608
Tyr *	
505	

<210> 16
 <211> 505
 <212> PRT
 <213> Homo Sapiens

<400> 16

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20 25 30	
Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val	
35 40 45	
Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro	
50 55 60	
Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp	
65 70 75 80	
Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp	
85 90 95	
Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser	
100 105 110	
Pro Pro Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu	
115 120 125	
Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp	
130 135 140	
Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys	
145 150 155 160	
Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys	

				165					170					175					
Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	Lys	Cys	Gln	Tyr				
			180						185				190						
Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn	Ala	Ile				
		195					200					205							
Arg	Phe	Gly	Arg	Met	Pro	Gln	Ala	Glu	Lys	Glu	Lys	Leu	Leu	Ala	Glu				
	210					215					220								
Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp	Leu	Arg				
225				230						235				240					
Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser	Phe	Pro	Leu				
			245					250					255						
Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	Lys	Thr	Thr	Asp	Lys				
		260					265					270							
Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	Met	Met	Gly	Glu	Asp				
	275					280				285									
Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln	Ser	Lys	Glu				
	290				295					300									
Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	Val	Glu	Ala				
305				310					315					320					
Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	Pro	Gly	Phe	Val	Asn				
		325						330				335							
Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	Val	His	Glu				
		340					345					350							
Ile	Ile	Tyr	Thr	Met	Leu	Ala	Ser	Leu	Met	Asn	Lys	Asp	Gly	Val	Leu				
	355					360						365							
Ile	Ser	Glu	Gly	Gln	Gly	Phe	Met	Thr	Arg	Glu	Phe	Leu	Lys	Ser	Leu				
	370				375					380									
Arg	Lys	Pro	Phe	Gly	Asp	Phe	Met	Glu	Pro	Lys	Phe	Glu	Phe	Ala	Val				
385				390					395					400					
Lys	Phe	Asn	Ala	Leu	Glu	Leu	Asp	Asp	Ser	Asp	Leu	Ala	Ile	Phe	Ile				
		405						410				415							
Ala	Val	Ile	Ile	Leu	Ser	Gly	Asp	Arg	Pro	Gly	Leu	Leu	Asn	Val	Lys				
	420						425					430							
Pro	Ile	Glu	Asp	Ile	Gln	Asp	Asn	Leu	Leu	Gln	Ala	Leu	Glu	Leu	Gln				
	435					440						445							
Leu	Lys	Leu	Asn	His	Pro	Glu	Ser	Ser	Gln	Leu	Phe	Ala	Lys	Leu	Leu				
	450					455					460								
Gln	Lys	Met	Thr	Asp	Leu	Arg	Gln	Ile	Val	Thr	Glu	His	Val	Gln	Leu				
465				470						475				480					
Leu	Gln	Val	Ile	Lys	Lys	Thr	Glu	Thr	Asp	Met	Ser	Leu	His	Pro	Leu				
		485						490				495							
Leu	Gln	Glu	Ile	Tyr	Lys	Asp	Leu	Tyr											
		500					505												

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 <212> DNA
 <213> Homo Sapiens

<400> 17
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<210> 18
 <211> 18
 <212> DNA
 <213> Homo Sapiens

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<400> 18
gctcaacagc accctgga                                     18

<210> 19
<211> 20
<212> DNA
<213> Homo Sapiens

<400> 19
gcaacctctc gactcaccag                                    20

<210> 20
<211> 20
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<213> Homo Sapiens

<400> 20
caaaggagtg ggagtgggtct                                  20

<210> 21
<211> 20
<212> DNA
<213> Homo Sapiens

<400> 21
cattacggag agatccacgg                                    20

<210> 22
<211> 2596
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (161)...(2596)

<400> 22
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tgagggcctg cagccggccg gccagggcag cggcaggcgc ggcccgacc tacgggagga      120
agccccgagc cctcggcggg ctgcgagcga ctccccggcg atg cct cac aac tcc      175
                                         Met Pro His Asn Ser
                                         1             5

atc aga tct ggc cat gga ggg ctg aac cag ctg gga ggg gcc ttt gtg      223
Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu Gly Gly Ala Phe Val
                        10                15                20

aat ggc aga cct ctg ccg gaa gtg gtc cgc cag cgc atc gta gac ctg      271
Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln Arg Ile Val Asp Leu
                        25                30                35

gcc cac cag ggt gta agg ccc tgc gac atc tct cgc cag ctg cgc gtc      319
Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser Arg Gln Leu Arg Val
                        40                45                50

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Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg Tyr Tyr Glu Thr Gly	
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Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys Pro Lys Val Ala Thr	
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ccc aag gtg gtg gag aag att ggg gac tac aaa cgc cag aac cct acc	463
Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys Arg Gln Asn Pro Thr	
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atg ttt gcc tgg gag atc cga gac cgg ctc ctg gct gag ggc gtc tgt	511
Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu Ala Glu Gly Val Cys	
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gac aat gac act gtg ccc agt gtc agc tcc att aat aga atc atc cgg	559
Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile Asn Arg Ile Ile Arg	
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Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met Asp Ser Cys Val Ala	
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Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile Pro Ser Ser Ala Val	
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Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly Ser Asp Lys Arg Lys	
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Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu Ser Ile Asp Ser Gln	
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Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg Thr Asp Ala Phe Ser	
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Gln His His Leu Glu Pro Leu Glu Cys Pro Phe Glu Arg Gln His Tyr	
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Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys Gly Glu Gln Gly Leu	
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tac ccg ctg ccc ttg ctc aac agc acc ctg gac gac ggg aag gcc acc	991
Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp Asp Gly Lys Ala Thr	
265 270 275	

ctg acc cct tcc aac acg cca	ctg ggg cgc aac ctc	tcg act cac cag	1039
Leu Thr Pro Ser Asn Thr Pro	Leu Gly Arg Asn Leu	Ser Thr His Gln	
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acc tac ccc gtg gtg gca ggg cga gag atg gtg ggg ccc acg ctg ccc			1087
Thr Tyr Pro Val Val Ala Gly Arg Glu Met Val Gly Pro Thr Leu Pro			
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Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly Ser Tyr Ala Ser			
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tct gcc atc gca ggc atg gtg gca gaa atg acc atg gtt gac aca gag			1183
Ser Ala Ile Ala Gly Met Val Ala Glu Met Thr Met Val Asp Thr Glu			
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atg cca ttc tgg ccc acc aac ttt ggg atc agc tcc gtg gat ctc tcc			1231
Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val Asp Leu Ser			
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gta atg gaa gac cac tcc cac tcc ttt gat atc aag ccc ttc act act			1279
Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr			
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gtt gac ttc tcc agc att tct act cca cat tac gaa gac att cca ttc			1327
Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe			
	375	380	385
aca aga aca gat cca gtg gtt gca gat tac aag tat gac ctg aaa ctt			1375
Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu			
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caa gag tac caa agt gca atc aaa gtg gag cct gca tct cca cct tat			1423
Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro Tyr			
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tat tct gag aag act cag ctc tac aat aag cct cat gaa gag cct tcc			1471
Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser			
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aac tcc ctc atg gca att gaa tgt cgt gtc tgt gga gat aaa gct tct			1519
Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys Ala Ser			
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Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe			
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cgg aga aca atc aga ttg aag ctt atc tat gac aga tgt gat ctt aac			1615
Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys Asp Leu Asn			
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tgt cgg atc cac aaa aaa agt aga aat aaa tgt cag tac tgt cgg ttt			1663
Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr Cys Arg Phe			
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Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile Arg Phe Gly	
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cgg atg cca cag gcc gag aag gag aag ctg ttg gcg gag atc tcc agt	1759
Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu Ile Ser Ser	
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Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg Ala Leu Ala	
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Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu Thr Lys Ala	
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Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys Ser Pro Phe	
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Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp Lys Ile Lys	
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Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile	
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cgc atc ttt cag ggc tgc cag ttt cgc tcc gtg gag gct gtg cag gag	2047
Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu	
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atc aca gag tat gcc aaa agc att cct ggt ttt gta aat ctt gac ttg	2095
Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu	
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Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr	
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aca atg ctg gcc tcc ttg atg aat aaa gat ggg gtt ctc ata tcc gag	2191
Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu	
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Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro	
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Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn	
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Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala Val Ile	
710 715 720 725	

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Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys Pro Ile Glu	
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Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu Leu Gln Val	
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Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu Leu Gln Glu	
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Ile Tyr Lys Asp Leu Tyr *	
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35 40 45	
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg	
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Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys	
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Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys	
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Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu	
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Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile	
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Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu	
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Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly	
180 185 190	
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu	
195 200 205	

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Asp	Gly	Lys	Ala	Thr	Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn
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Leu	Ser	Thr	His	Gln	Thr	Tyr	Pro	Val	Val	Ala	Gly	Arg	Glu	Met	Val
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Gly	Ser	Tyr	Ala	Ser	Ser	Ala	Ile	Ala	Gly	Met	Val	Ala	Glu	Met	Thr
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Met	Val	Asp	Thr	Glu	Met	Pro	Phe	Trp	Pro	Thr	Asn	Phe	Gly	Ile	Ser
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Ser	Val	Asp	Leu	Ser	Val	Met	Glu	Asp	His	Ser	His	Ser	Phe	Asp	Ile
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Lys	Pro	Phe	Thr	Thr	Val	Asp	Phe	Ser	Ser	Ile	Ser	Thr	Pro	His	Tyr
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Glu	Asp	Ile	Pro	Phe	Thr	Arg	Thr	Asp	Pro	Val	Val	Ala	Asp	Tyr	Lys
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Tyr	Asp	Leu	Lys	Leu	Gln	Glu	Tyr	Gln	Ser	Ala	Ile	Lys	Val	Glu	Pro
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His	Glu	Glu	Pro	Ser	Asn	Ser	Leu	Met	Ala	Ile	Glu	Cys	Arg	Val	Cys
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Arg	Cys	Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	Lys	Cys
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Gln	Tyr	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn
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Ala	Glu	Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp
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Leu	Arg	Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser	Phe
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Pro	Leu	Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	Lys	Thr	Thr
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Asp	Lys	Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	Met	Met	Gly
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Glu	Asp	Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln	Ser
	595						600					605			
Lys	Glu	Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	Val
	610					615					620				
Glu	Ala	Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	Pro	Gly	Phe
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Val	Asn	Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	Val
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Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys
675 680 685
Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe
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Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile
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Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu
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Met Pro His Asn Ser
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atc aga tct ggc cat gga ggg ctg aac cag ctg gga ggg gcc ttt gtg 223
Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu Gly Gly Ala Phe Val
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Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln Arg Ile Val Asp Leu
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Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys Pro Lys Val Ala Thr
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Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu Ala Glu Gly Val Cys	
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Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile Asn Arg Ile Ile Arg	
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Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met Asp Ser Cys Val Ala	
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Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg Thr Asp Ala Phe Ser	
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Gln His His Leu Glu Pro Leu Glu Cys Pro Phe Glu Arg Gln His Tyr	
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Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys Gly Glu Gln Gly Leu	
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Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp Asp Gly Lys Ala Thr	
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Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro Leu Ala Ile Lys Gln	
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2711

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Gly	Gly	Ala	Phe	Val	Asn	Gly	Arg	Pro	Leu	Pro	Glu	Val	Val	Arg	Gln
		20						25					30		
Arg	Ile	Val	Asp	Leu	Ala	His	Gln	Gly	Val	Arg	Pro	Cys	Asp	Ile	Ser
	35						40					45			
Arg	Gln	Leu	Arg	Val	Ser	His	Gly	Cys	Val	Ser	Lys	Ile	Leu	Gly	Arg
	50					55					60				
Tyr	Tyr	Glu	Thr	Gly	Ser	Ile	Arg	Pro	Gly	Val	Ile	Gly	Gly	Ser	Lys
65					70					75				80	
Pro	Lys	Val	Ala	Thr	Pro	Lys	Val	Val	Glu	Lys	Ile	Gly	Asp	Tyr	Lys
				85					90					95	
Arg	Gln	Asn	Pro	Thr	Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	Arg	Leu	Leu
		100						105					110		
Ala	Glu	Gly	Val	Cys	Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	Ser	Ser	Ile
		115					120					125			
Asn	Arg	Ile	Ile	Arg	Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met
	130					135					140				
Asp	Ser	Cys	Val	Ala	Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile
145					150					155				160	
Pro	Ser	Ser	Ala	Val	Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu
			165						170					175	
Gly	Ser	Thr	Tyr	Ser	Ile	Asn	Gly	Leu	Leu	Gly	Ile	Ala	Gln	Pro	Gly
		180					185						190		
Ser	Asp	Lys	Arg	Lys	Met	Asp	Asp	Ser	Asp	Gln	Asp	Ser	Cys	Arg	Leu
	195					200					205				
Ser	Ile	Asp	Ser	Gln	Ser	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg
	210					215					220				
Thr	Asp	Ala	Phe	Ser	Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe
225					230					235				240	
Glu	Arg	Gln	His	Tyr	Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys
			245					250					255		
Gly	Glu	Gln	Gly	Leu	Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp
		260					265					270			
Asp	Gly	Lys	Ala	Thr	Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn
	275					280					285				
Leu	Ser	Thr	His	Gln	Thr	Tyr	Pro	Val	Val	Ala	Asp	Pro	His	Ser	Pro
	290					295					300				
Leu	Ala	Ile	Lys	Gln	Glu	Thr	Pro	Glu	Val	Ser	Ser	Ser	Ser	Ser	Thr
305					310				315					320	
Pro	Cys	Ser	Leu	Ser	Ser	Ser	Ala	Leu	Leu	Asp	Leu	Gln	Gln	Val	Gly
			325						330				335		
Ser	Gly	Val	Pro	Pro	Phe	Asn	Ala	Phe	Pro	His	Ala	Ala	Ser	Val	Tyr
		340					345					350			
Gly	Gln	Phe	Thr	Gly	Gln	Ala	Leu	Leu	Ser	Gly	Arg	Glu	Met	Val	Gly
		355				360					365				
Pro	Thr	Leu	Pro	Gly	Tyr	Pro	Pro	His	Ile	Pro	Thr	Ser	Gly	Gln	Gly
	370					375					380				

Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Gly Ser Glu Tyr
 385 390 395 400
 Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala
 405 410 415
 Trp Gly Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Tyr Ser
 420 425 430
 Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp
 435 440 445
 His Leu
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 ggtcggcctc gaggacaccg gagaggggag ccacgccgcc gtggccgcag aa atg acc 178
 Met Thr
 1
 atg gtt gac aca gag atc gca ttc tgg ccc acc aac ttt ggg atc agc 226
 Met Val Asp Thr Glu Ile Ala Phe Trp Pro Thr Asn Phe Gly Ile Ser
 5 10 15
 tcc gtg gat ctc tcc gta atg gaa gac cac tcc cac tcc ttt gat atc 274
 Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile
 20 25 30
 aag ccc ttc act act gtt gac ttc tcc agc att tct act cca cat tac 322
 Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr
 35 40 45 50
 gaa gac att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag 370
 Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys
 55 60 65
 tat gac ctg aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct 418
 Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro
 70 75 80
 gca tct cca cct tat tat tct gag aag act cag ctc tac aat aag cct 466
 Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro
 85 90 95
 cat gaa gag cct tcc aac tcc ctc atg gca att gaa tgt cgt gtc tgt 514
 His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys
 100 105 110
 gga gat aaa gct tct gga ttt cac tat gga gtt cat gct tgt gaa gga 562

Gly 115	Asp	Lys	Ala	Ser	Gly 120	Phe	His	Tyr	Gly 125	Val	His	Ala	Cys	Glu	Gly 130	
tgc	aag	ggt	ttc	ttc	cgg	aga	aca	atc	aga	ttg	aag	ctt	atc	tat	gac	610
Cys	Lys	Gly	Phe	Phe	Arg	Arg	Thr	Ile	Arg	Leu	Lys	Leu	Ile	Tyr	Asp	
				135					140					145		
aga	tgt	gat	ctt	aac	tgt	cgg	atc	cac	aaa	aaa	agt	aga	aat	aaa	tgt	658
Arg	Cys	Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	Lys	Cys	
			150				155						160			
cag	tac	tgt	cgg	ttt	cag	aaa	tgc	ctt	gca	gtg	ggg	atg	tct	cat	aat	706
Gln	Tyr	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn	
		165					170					175				
gcc	atc	agg	ttt	ggg	cgg	atc	gca	cag	gcc	gag	aag	gag	aag	ctg	ttg	754
Ala	Ile	Arg	Phe	Gly	Arg	Ile	Ala	Gln	Ala	Glu	Lys	Glu	Lys	Leu	Leu	
	180					185				190						
gcg	gag	atc	tcc	agt	gat	atc	gac	cag	ctg	aat	cca	gag	tcc	gct	gac	802
Ala	Glu	Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp	
195					200					205					210	
ctc	cgt	cag	gcc	ctg	gca	aaa	cat	ttg	tat	gac	tca	tac	ata	aag	tcc	850
Leu	Arg	Gln	Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser	
				215					220					225		
ttc	ccg	ctg	acc	aaa	gca	aag	gcg	agg	gcg	atc	ttg	aca	gga	aag	aca	898
Phe	Pro	Leu	Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	Lys	Thr	
			230					235					240			
aca	gac	aaa	tca	cca	ttc	gtt	atc	tat	gac	atg	aat	tcc	tta	atg	atg	946
Thr	Asp	Lys	Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	Met	Met	
		245					250					255				
gga	gaa	gat	aaa	atc	aag	ttc	aaa	cac	atc	acc	ccc	ctg	cag	gag	cag	994
Gly	Glu	Asp	Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln	
	260					265					270					
agc	aaa	gag	gtg	gcc	atc	cgc	atc	ttt	cag	ggc	tgc	cag	ttt	cgc	tcc	1042
Ser	Lys	Glu	Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	
275					280					285					290	
gtg	gag	gct	gtg	cag	gag	atc	aca	gag	tat	gcc	aaa	agc	att	cct	ggt	1090
Val	Glu	Ala	Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	Pro	Gly	
				295					300					305		
ttt	gta	aat	ctt	gac	ttg	aac	gac	caa	gta	act	ctc	ctc	aaa	tat	gga	1138
Phe	Val	Asn	Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	
			310					315					320			
gtc	cac	gag	atc	att	tac	aca	atg	ctg	gcc	tcc	ttg	atg	aat	aaa	gat	1186
Val	His	Glu	Ile	Ile	Tyr	Thr	Met	Leu	Ala	Ser	Leu	Met	Asn	Lys	Asp	
		325					330					335				
ggg	gtt	ctc	ata	tcc	gag	ggc	caa	ggc	ttc	atg	aca	agg	gag	ttt	cta	1234

Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu	
340 345 350	
aag agc ctg cga aag cct ttt ggt gac ttt atg gag ccc aag ttt gag	1282
Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu	
355 360 365 370	
ttt gct gtg aag ttc aat gca ctg gaa tta gat gac agc gac ttg gca	1330
Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala	
375 380 385	
ata ttt att gct gtc att att ctc agt gga gac cgc cca ggt ttg ctg	1378
Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu	
390 395 400	
aat gtg aag ccc att gaa gac att caa gac aac ctg cta caa gcc ctg	1426
Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu	
405 410 415	
gag ctc cag ctg aag ctg aac cac cct gag tcc tca cag ctg ttt gcc	1474
Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala	
420 425 430	
aag ctg ctc cag aaa atg aca gac ctc aga cag att gtc acg gaa cac	1522
Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His	
435 440 445 450	
gtg cag cta ctg cag gtg atc aag aag acg gag aca gac atg agt ctt	1570
Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu	
455 460 465	
cac ccg ctc ctg cag gag atc tac aag gac ttg tac tag cagagagtcc	1619
His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr *	
470 475	
tgagccactg ccaacatttc ccttcttcca gttgcactat tctgagggaa aatctgacca	1679
taagaaaattt actgtgaaaa agcgttttaa aaagaaaagg gtttagaata tgatctattt	1739
tatgcatatt gtttataaag acacatttac aatttacttt taatattaaa aattaccata	1799
ttatgaaatt gc	1811

<210> 27
 <211> 478
 <212> PRT
 <213> Homo Sapiens

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Ile Ser Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe	
20 25 30	
Asp Ile Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro	
35 40 45	
His Tyr Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp	
50 55 60	
Tyr Lys Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val	
65 70 75 80	

Glu	Pro	Ala	Ser	Pro	Pro	Tyr	Tyr	Ser	Glu	Lys	Thr	Gln	Leu	Tyr	Asn	
			85						90					95		
Lys	Pro	His	Glu	Glu	Pro	Ser	Asn	Ser	Leu	Met	Ala	Ile	Glu	Cys	Arg	
			100					105					110			
Val	Cys	Gly	Asp	Lys	Ala	Ser	Gly	Phe	His	Tyr	Gly	Val	His	Ala	Cys	
		115					120					125				
Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Thr	Ile	Arg	Leu	Lys	Leu	Ile	
	130				135					140						
Tyr	Asp	Arg	Cys	Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	
145					150					155					160	
Lys	Cys	Gln	Tyr	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	
			165						170					175		
His	Asn	Ala	Ile	Arg	Phe	Gly	Arg	Ile	Ala	Gln	Ala	Glu	Lys	Glu	Lys	
		180						185					190			
Leu	Leu	Ala	Glu	Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	
		195					200					205				
Ala	Asp	Leu	Arg	Gln	Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	
	210					215					220					
Lys	Ser	Phe	Pro	Leu	Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	
225					230					235					240	
Lys	Thr	Thr	Asp	Lys	Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	
			245						250					255		
Met	Met	Gly	Glu	Asp	Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	
		260						265					270			
Glu	Gln	Ser	Lys	Glu	Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	
		275					280					285				
Arg	Ser	Val	Glu	Ala	Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	
	290					295					300					
Pro	Gly	Phe	Val	Asn	Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	
305					310					315					320	
Tyr	Gly	Val	His	Glu	Ile	Ile	Tyr	Thr	Met	Leu	Ala	Ser	Leu	Met	Asn	
			325						330					335		
Lys	Asp	Gly	Val	Leu	Ile	Ser	Glu	Gly	Gln	Gly	Phe	Met	Thr	Arg	Glu	
		340						345					350			
Phe	Leu	Lys	Ser	Leu	Arg	Lys	Pro	Phe	Gly	Asp	Phe	Met	Glu	Pro	Lys	
		355					360					365				
Phe	Glu	Phe	Ala	Val	Lys	Phe	Asn	Ala	Leu	Glu	Leu	Asp	Asp	Ser	Asp	
	370					375					380					
Leu	Ala	Ile	Phe	Ile	Ala	Val	Ile	Ile	Leu	Ser	Gly	Asp	Arg	Pro	Gly	
385					390					395					400	
Leu	Leu	Asn	Val	Lys	Pro	Ile	Glu	Asp	Ile	Gln	Asp	Asn	Leu	Leu	Gln	
			405						410					415		
Ala	Leu	Glu	Leu	Gln	Leu	Lys	Leu	Asn	His	Pro	Glu	Ser	Ser	Gln	Leu	
		420						425					430			
Phe	Ala	Lys	Leu	Leu	Gln	Lys	Met	Thr	Asp	Leu	Arg	Gln	Ile	Val	Thr	
		435					440					445				
Glu	His	Val	Gln	Leu	Leu	Gln	Val	Ile	Lys	Lys	Thr	Glu	Thr	Asp	Met	
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Ser	Leu	His	Pro	Leu	Leu	Gln	Glu	Ile	Tyr	Lys	Asp	Leu	Tyr			
465					470					475						

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 <212> DNA
 <213> Homo Sapiens

<400> 28
gccaccaagt ccctgagtcc 20

<210> 29
<211> 19
<212> DNA
<213> Homo Sapiens

<400> 29
gacctacggg aggaagccc 19

<210> 30
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<212> DNA
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<400> 30
gcggacccaa gcagtgag 18

<210> 31
<211> 21
<212> DNA
<213> Homo Sapiens

<400> 31
tttcttatgg tcagattttc c 21

<210> 32
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<212> DNA
<213> Homo Sapiens

<400> 32
accagaaag cgattccttc a 21

<210> 33
<211> 20
<212> DNA
<213> Homo Sapiens

<400> 33
atgggtgaaa ctctgggaga 20

<210> 34
<211> 20
<212> DNA
<213> Homo Sapiens

<400> 34
ttgctgcaga tccaaaaagg 20

<210> 35
<211> 20
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<400> 35
gaggaagggg tggagctaga

20

<210> 36
<211> 537
<212> DNA
<213> Homo Sapiens

<220>
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<222> (85)...(85)
<223> n = A or T or C or G or other

<400> 36
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ttc act gat aca ctg tct gca aac ata tca caa gaa nat cct cac tca 96
ccc ttc gcc ata aag cag gaa acc ccc gag gtg tcc agt tct agc tcc 144
acc cct tcc tct tta tct agc tcc gcc ttt ttg gat ctg cag caa gtc 192
ggc tcc ggg gtc ccg ccc ttc aat gcc ttt ccc cat gct gcc tcc gtg 240
tac ggg cag ttc acg ggc cag gcc ctc ctc tca ggg cga gag atg gtg 288
ggg ccc acg ctg ccc gga tac cca ccc cac atc ccc acc agc gga cag 336
ggc agc tat gcc tcc tct gcc atc gca ggc atg gtg gca gga agt gaa 384
tac tct ggc aat gcc tat ggc cac acc ccc tac tcc tcc tac agc gag 432
gcc tgg cgc ttc ccc aac tcc agc ttg ctg agt tcc cca tat tat tac 480
agt tcc aca tca agg ccg agt gca ccg ccc acc act gcc acg gcc ttt 528
gac cat ctg 537

<210> 37
<211> 348
<212> DNA
<213> Homo Sapiens

<220>
<221> Unknown
<222> (85)...(85)
<223> n = A or T or C or G or other

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ctgtctgcaa acatatcaca agaanggcga gagatgggtg ggcccacgct gcccgatac 120
ccacccaca tccccaccag cggacagggc agctatgcct cctctgccat cgcaggcatg 180
gtggcaggaa gtgaatactc tggcaatgcc tatggccaca cccctactc ctctacagc 240
gaggcctggc gcttccccaa ctccagcttg ctgagttccc catattatta cagttccaca 300
tcaaggccga gtgcaccgcc caccactgcc acggcctttg accatctg 348

<210> 38
<211> 246
<212> DNA
<213> Homo Sapiens

<220>
<221> Unknown
<222> (85)...(85)
<223> n = A or T or C or G or other

<400> 38

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ctgtctgcaa acatatcaca agaangaagt gaatactctg gcaatgccta tggccacacc      120
ccctactcct cctacagcga ggctgggcgc ttccccaact ccagcttgct gagttcccca      180
tattattaca gttccacatc aaggccgagt gcaccgccca ccactgccac ggcctttgac      240
catctg                                         246

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<210> 39
<211> 178
<212> PRT
<213> Homo Sapiens

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<220>
<221> Unknown
<222> (29)...(29)
<223> Xaa = any amino acid

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<400> 39
Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
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Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Xaa Pro His Ser
          20          25          30
Pro Phe Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser Ser Ser
          35          40          45
Thr Pro Ser Ser Leu Ser Ser Ser Ala Phe Leu Asp Leu Gln Gln Val
          50          55          60
Gly Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala Ser Val
65          70          75          80
Tyr Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Gly Arg Glu Met Val
          85          90          95
Gly Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln
          100          105          110
Gly Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Gly Ser Glu
          115          120          125
Tyr Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu
          130          135          140
Ala Trp Arg Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Tyr
          145          150          155          160
Ser Ser Thr Ser Arg Pro Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp
          165          170          175
His Leu

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<210> 40
<211> 116
<212> PRT
<213> Homo Sapiens

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<220>
<221> Unknown
<222> (29)...(29)
<223> Xaa = any amino acid

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<400> 40
Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
 1          5          10          15
Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Xaa Arg Glu Met

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Val	Gly	Pro	Thr	Leu	Pro	Gly	Tyr	Pro	Pro	His	Ile	Pro	Thr	Ser	Gly
		35					40					45			
Gln	Gly	Ser	Tyr	Ala	Ser	Ser	Ala	Ile	Ala	Gly	Met	Val	Ala	Gly	Ser
	50					55					60				
Glu	Tyr	Ser	Gly	Asn	Ala	Tyr	Gly	His	Thr	Pro	Tyr	Ser	Ser	Tyr	Ser
65					70					75					80
Glu	Ala	Trp	Arg	Phe	Pro	Asn	Ser	Ser	Leu	Leu	Ser	Ser	Pro	Tyr	Tyr
				85					90				95		
Tyr	Ser	Ser	Thr	Ser	Arg	Pro	Ser	Ala	Pro	Pro	Thr	Thr	Ala	Thr	Ala
			100					105					110		
Phe	Asp	His	Leu												
			115												

<210> 41
 <211> 82
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> Unknown
 <222> (29)...(29)
 <223> Xaa = any amino acid

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Phe	Thr	Asp	Thr	Leu	Ser	Ala	Asn	Ile	Ser	Gln	Glu	Xaa	Ser	Glu	Tyr
			20				25					30			
Ser	Gly	Asn	Ala	Tyr	Gly	His	Thr	Pro	Tyr	Ser	Ser	Tyr	Ser	Glu	Ala
	35					40						45			
Trp	Arg	Phe	Pro	Asn	Ser	Ser	Leu	Leu	Ser	Ser	Pro	Tyr	Tyr	Tyr	Ser
	50				55						60				
Ser	Thr	Ser	Arg	Pro	Ser	Ala	Pro	Pro	Thr	Thr	Ala	Thr	Ala	Phe	Asp
65					70				75						80
His	Leu														

<210> 42
 <211> 43
 <212> DNA
 <213> Homo Sapiens

<220>
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 <222> (22)...(22)
 <223> n = A or T or C or G or other

<221> CDS
 <222> (1)...(43)

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1				5				10						
Ser	Ala	Asn	Ile	Ser	Gln	Glu	Xaa	Pro	His	Ser	Pro	Phe	Ala	

<210> 43
 <211> 14
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> Unknown
 <222> (8)...(8)
 <223> Xaa = any amino acid

<400> 43
 Ser Ala Asn Ile Ser Gln Glu Xaa Pro His Ser Pro Phe Ala
 1 5 10

<210> 44
 <211> 43
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> Unknown
 <222> (22)...(22)
 <223> n = A or T or C or G or other

<221> CDS
 <222> (1)...(43)

<400> 44
 tct gca aac ata tca caa gaa ngg cga gag atg gtg ggg ccc a
 Ser Ala Asn Ile Ser Gln Glu Xaa Arg Glu Met Val Gly Pro
 1 5 10

43

<210> 45
 <211> 14
 <212> PRT
 <213> Homo Sapiens

<220>
 <221> Unknown
 <222> (8)...(8)
 <223> Xaa = any amino acid

<400> 45
 Ser Ala Asn Ile Ser Gln Glu Xaa Arg Glu Met Val Gly Pro
 1 5 10

<210> 46
 <211> 43
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> Unknown
 <222> (22)...(22)

<223> n = a or T or C or G or other

<221> CDS

<222> (1)...(43)

<400> 46

tct gca aac ata tca caa gaa nga agt gaa tac tct ggc aat g
Ser Ala Asn Ile Ser Gln Glu Xaa Ser Glu Tyr Ser Gly Asn
1 5 10

43

<210> 47

<211> 14

<212> PRT

<213> Homo Sapiens

<220>

<221> Unknown

<222> (8)...(8)

<223> Xaa = any amino acid

<400> 47

Ser Ala Asn Ile Ser Gln Glu Xaa Ser Glu Tyr Ser Gly Asn
1 5 10